GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:33:36 ; Search time 176 Seconds
(without alignments)
480.074 Million cell updates/sec

Title: US-09-786-867C-5
Perfect score: 893
Sequence: 1 MTTASTSQVRQNYHQDSEAA.....PRRRKRPHSIPTPILIFRSP 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	890	99.7	165	2	Q8TD27	Q8td27 homo sapien
2	615.5	68.9	232	2	Q6NS36	Q6ns36 homo sapien
3	610.5	68.4	182	1	FRIH_HUMAN	P02794 homo sapien
4	605.5	67.8	183	2	Q6NZ44	Q6nz44 homo sapien
5	589.5	66.0	182	1	FRIH_TRIVU	Q9xt73 trichosurus
6	589.5	66.0	183	2	Q95MP7	Q95mp7 canis famil
7	586.5	65.7	182	2	Q920K4	Q920k4 cavia porce
8	585	65.5	197	2	Q6P9V2	Q6p9v2 rattus norv
9	583.5	65.3	220	2	Q66HI5	Q66hi5 rattus norv
10	583.5	65.3	229	2	Q6AYV6	Q6ayv6 rattus norv
11	580.5	65.0	185	1	FRIH_CRIGR	P29389 cricetulus
12	575.5	64.4	181	1	FRIH_MOUSE	P09528 mus musculu
13	573.5	64.2	181	1	FRIH_RAT	P19132 rattus norv
14	570.5	63.9	182	2	Q8MIP0	Q8mip0 equus cabal
15	560.5	62.8	170	1	FRIH_SHEEP	P18685 ovis aries
16	560.5	62.8	179	1	FRIH_CHICK	P08267 gallus gall
17	560.5	62.8	180	1	FRIH_BOVIN	O46414 bos taurus
18	560.5	62.8	181	2	Q6PRV1	Q6prv1 coturnix co
19	516.5	57.8	177	2	Q7ZXM8	Q7zxm8 xenopus lae
20	515.5	57.7	177	2	Q6DDB5	Q6ddb5 xenopus tro
21	514.5	57.6	169	2	Q8HZP4	Q8hzp4 bos taurus
22	514.5	57.6	177	1	FRH3_XENLA	Q7sxa6 xenopus lae
23	508.5	56.9	180	1	FRIH_PIG	P19130 sus scrofa
24	500	56.0	157	2	Q7ZZT8	Q7zzt8 oreochromis
25	499.5	55.9	164	1	FRIH_RABIT	P25915 oryctolagus
26	494	55.3	100	2	Q862J4	Q862j4 bos taurus
27	494	55.3	242	2	Q8N4E7	Q8n4e7 homo sapien
28	488.5	54.7	152	2	Q6EEB2	Q6eeb2 latimeria c
29	480	53.8	132	2	Q6Y241	Q6y241 pagrus majo
30	479	53.6	237	2	Q9D5F4	Q9d5f4 mus musculu
31	477	53.4	262	2	Q9D5H4	Q9d5h4 mus musculu
32	475	53.2	177	1	FRIH_SALSA	P49946 salmo salar
33	469	52.5	177	2	Q9DDT0	Q9ddt0 brachydanio
34	460.5	51.6	175	2	Q801J6	Q801j6 scyliorhinu
35	458	51.3	177	2	Q66HX7	Q66hx7 brachydanio
36	457	51.2	92	2	Q862D5	Q862d5 bos taurus
37	456.5	51.1	127	2	Q862R4	Q862r4 bos taurus
38	453	50.7	176	2	Q98TT0	Q98tt0 oncorhynchu
39	441	49.4	156	2	Q6EEB1	Q6eeb1 protopterus
40	440	49.3	177	2	Q801J5	Q801j5 petromyzon
41	439	49.2	173	1	FRIS_LYMST	P42577 lymnaea sta
42	436	48.8	134	2	Q86QN8	Q86qn8 branchiosto
43	436	48.8	172	2	Q6WNW7	Q6wnw7 branchiosto
44	435.5	48.8	149	2	Q9GMG9	Q9gmg9 macaca mula
45	435.5	48.8	174	2	Q86LZ3	Q861z3 branchiosto

ALIGNMENTS

RESULT 1
Q8TD27
ID Q8TD27 PRELIMINARY; PRT; 165 AA.
AC Q8TD27;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Placenta immunoregulatory factor PLIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21935397; PubMed=11821435; DOI=10.1074/jbc.M200956200;
RA Moroz C., Traub L., Maymon R., Zahalka M.A.;
RT "PLIF, a novel human ferritin subunit from placenta with
RT immunosuppressive activity.";
RL J. Biol. Chem. 277:12901-12905(2002).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AY033611; AAK55486.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0019900; F:kinase binding; NAS.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 165 AA; 19490 MW; C4849C853FCABAB6 CRC64;

Query Match 99.7%; Score 890; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.1e-71;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQS 60

Qy         61 HEERQHAEKLMKLQNQRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNQSLLEFPS 120
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HEEREHAEKLMKLQNQRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNQSLLEFPS 120

Qy        121 PISPSPSCWHHYTTNRPQPQHHLLRPRRRKRPHSIPTPILIFRSP 165
              |||||||||||||||||||||||||||||||||||||||||||||
Db        121 PISPSPSCWHHYTTNRPQPQHHLLRPRRRKRPHSIPTPILIFRSP 165
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